

# **DNA Fingerprinting of *Exiguobacterium* Strains with Insertion Sequence Elements: Implication for Astrobiology.**

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Nineteen strains of the low-GC gram-positive bacterium *Exiguobacterium* were isolated from markedly diverse environments including ancient Siberian permafrost and Greenland glacial ice, contemporary polar and temperate soils and lakes, hot springs, and food processing plants. The genome of *Exiguobacterium* sp. 255-15, isolated from 2-3 million years old Siberian permafrost was fully sequenced. The 2.9 Mb genome of this isolate includes 2977 candidate protein-coding sequences, 47 of which were assigned to putative transposases. Sequences representative of nine different transposase groups were then utilized as probes in Southern blots. Each of the putative transposase gene probes from ancient permafrost strain 255-15 were found to have highly conserved homologs in the genome of several other *Exiguobacterium* spp., not only from permafrost but also from remarkably diverse modern environments. Insertion sequences of the IS605/IS200 family were widely distributed among *Exiguobacterium* isolates and apparently found in multiple copies in the *Exiguobacterium* genomes. The number and location of the hybridization bands were unique and stable for each strain, and did not change due to growth at different temperatures or repetitive freeze-thaw cycles. In spite of high conservation of the transposase nucleotide sequences within the genus *Exiguobacterium*, these sequences had low similarity at the nucleotide level to transposases from other bacteria. Strain specificity of the hybridization patterns obtained with transposase probes suggests the potential of these genes for the generation of molecular subtyping tools for strain distinguishing. Furthermore, the insertion sequence elements may be used as biomarker for searching recognizable *Exiguobacterium* biosignatures in different terrestrial and extraterrestrial environments.